

PATENT
4760US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

de Baar et al.

Serial No.: To be assigned

Filed: February 16, 2001

For: REDUCING BACKGROUND IN
HYBRIDIZATION REACTIONS

Examiner: To be assigned

Group Art Unit: To be assigned

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PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

Sir:

Before examination and calculation of the filing fees, please amend the referenced application as follows:

IN THE CLAIMS

3. (Amended) The method according to claim 1 [or 2] in which the homologous probes are designed to detect point mutations in at least one target sequence.

5. (Amended) The method according to [any one of claims 1-4] claim 1, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

6. (Amended) The method according to [any one of claims 2-5] claim 2, wherein the mismatch in a nucleotide sequence is located between 2 and 20 nucleotides upstream or downstream of a point mutation.

7. (Amended) The method according to [any one of claims 1-6] claim 1 wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

8. (Amended) The method according to [any one of claims 1-7] claim 1 wherein the at least one of the non-linear probes is provided with a detectable moiety.

9. (Amended) The method according to [any one of claims 1-8] claim 1, further comprising amplifying a nucleic acid sequence.

13. (Amended) The set of mixed homologous probes of claim 11 [or 12] wherein said mismatch in a nucleic acid sequence is located 2-20 nucleotides upstream or downstream of said point mutation.

14. (Amended) The set of mixed homologous probes of [any one of claims 10-13] claim 10 wherein the set of mixed homologous probes have lengths between about 15 and about 50 nucleotides.

15. (Amended) The set of mixed homologous probes of [any one of claims 11-14] claim 11 wherein said set of mixed homologous probes are in a single container.

Please add the following claims:

21. The method according to claim 2 in which the homologous probes are designed to detect point mutations in at least one target sequence.

22. The method according to claim 2, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

23. The method according to claim 2 wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

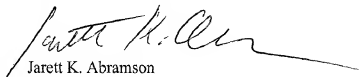
24. The method according to claim 2 wherein the at least one of the non-linear probes is provided with a detectable moiety.

25. The method according to claim 2, further comprising amplifying a nucleic acid sequence.

Remarks

The application is to be amended (without prejudice or disclaimer) as previously set forth which should not be viewed as narrowing or limiting the claims. The amendments are sought to conform the application to a form more consistent with Office practice by removing multiple dependencies. It is respectfully submitted that no new matter has been added by the amendments. If any questions remain after consideration of the instant amendments, the Office is kindly requested to contact applicants' attorney at the address or telephone number given herein.

Respectfully submitted,



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